



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:39 PM UTC

PDB ID : 6ZHS / pdb_00006zhs
Title : Uba1 bound to two E2 (Ubc13) molecules
Authors : Misra, M.; Schindelin, H.
Deposited on : 2020-06-23
Resolution : 2.35 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

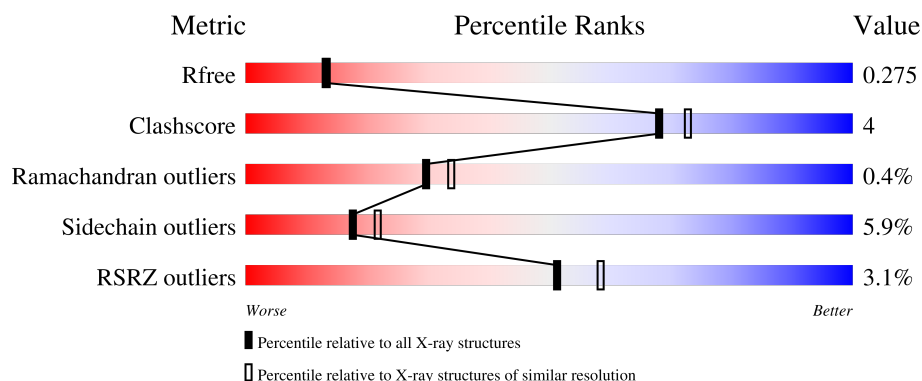
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1024	2% 85% 11% ..
2	B	154	4% 82% 14% ..
2	C	154	10% 87% 10% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 21003 atoms, of which 10317 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ubiquitin-activating enzyme E1 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	994	Total	C	H	N	O	S	0	3	0
			15631	5011	7768	1299	1530	23			

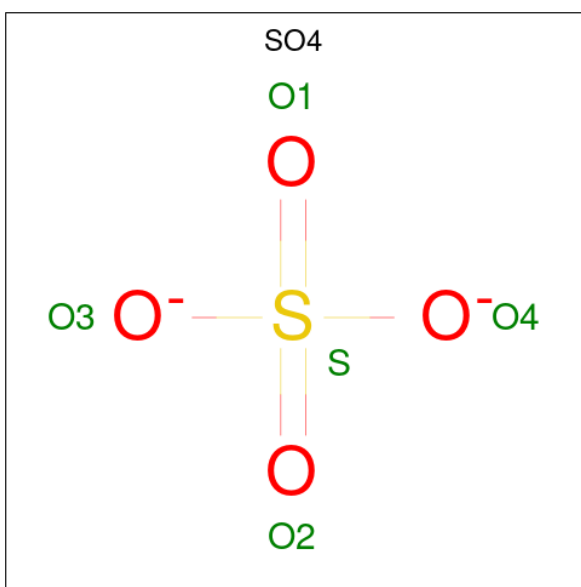
- Molecule 2 is a protein called Ubiquitin-conjugating enzyme E2 13.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	152	Total	C	H	N	O	S	0	6	0
			2526	804	1272	214	233	3			
2	C	151	Total	C	H	N	O	S	0	0	0
			2445	781	1229	204	228	3			

There are 2 discrepancies between the modelled and reference sequences:

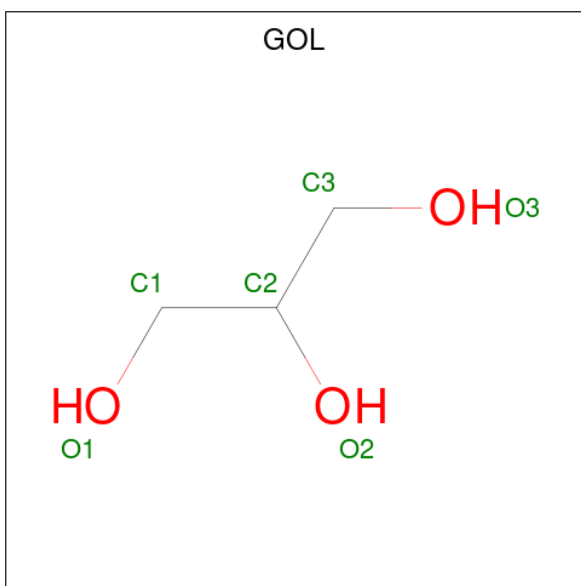
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP P52490
C	0	GLY	-	expression tag	UNP P52490

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		

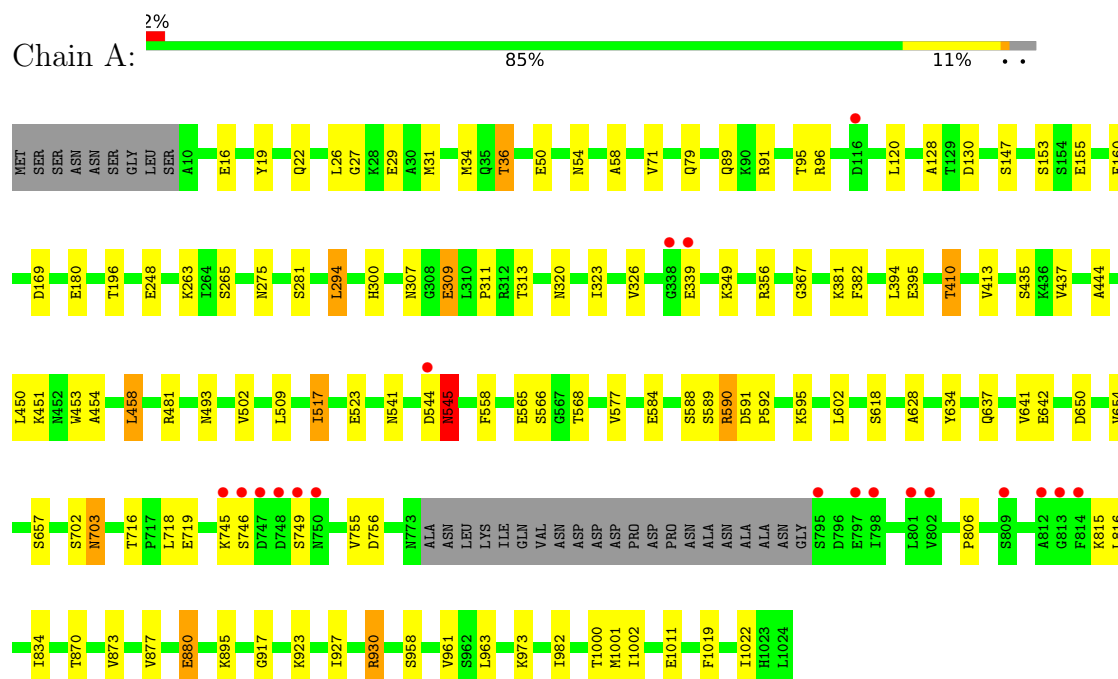
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	261	Total	O	0	0
			261	261		
5	B	21	Total	O	0	0
			21	21		
5	C	25	Total	O	0	0
			25	25		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Ubiquitin-activating enzyme E1 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	177.71Å 72.90Å 139.52Å 90.00° 112.43° 90.00°	Depositor
Resolution (Å)	24.92 – 2.35 24.92 – 2.35	Depositor EDS
% Data completeness (in resolution range)	66.2 (24.92-2.35) 66.1 (24.92-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.36Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.216 , 0.275 0.217 , 0.275	Depositor DCC
R_{free} test set	2266 reflections (3.29%)	wwPDB-VP
Wilson B-factor (Å ²)	26.9	Xtriage
Anisotropy	0.641	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	21003	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.32% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.14	0/8033	0.33	0/10869
2	B	0.14	0/1312	0.40	0/1784
2	C	0.15	0/1246	0.35	0/1696
All	All	0.14	0/10591	0.34	0/14349

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7863	7768	7758	58	0
2	B	1254	1272	1242	17	0
2	C	1216	1229	1231	5	0
3	A	10	0	0	0	0
4	A	36	48	48	2	0
5	A	261	0	0	0	0
5	B	21	0	0	0	0
5	C	25	0	0	0	0
All	All	10686	10317	10279	74	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 4.

All (74) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:493:ASN:HB3	1:A:517:ILE:HD11	1.68	0.74
1:A:71:VAL:HG22	1:A:91:ARG:HG2	1.74	0.69
2:B:4:LEU:HD13	2:B:5:PRO:HD3	1.76	0.67
1:A:444:ALA:HB1	1:A:870:THR:HG21	1.77	0.66
1:A:71:VAL:HG23	1:A:89:GLN:O	1.98	0.63
1:A:558:PHE:O	1:A:930:ARG:NH1	2.32	0.62
1:A:26:LEU:HD13	1:A:34:MET:HE1	1.81	0.62
1:A:294:LEU:HB3	1:A:326:VAL:HG13	1.82	0.61
1:A:958:SER:HB3	2:B:9:ILE:HD11	1.82	0.61
1:A:413:VAL:HG12	1:A:413:VAL:O	2.01	0.59
1:A:702:SER:O	1:A:703:ASN:HB2	2.03	0.59
1:A:544[B]:ASP:O	1:A:545[B]:ASN:CB	2.51	0.59
1:A:963:LEU:HB2	2:B:32:LEU:HD11	1.86	0.58
1:A:958:SER:CB	2:B:9:ILE:HD11	2.33	0.58
1:A:517:ILE:O	1:A:517:ILE:HG23	2.04	0.58
1:A:169:ASP:O	1:A:265:SER:OG	2.21	0.56
1:A:450:LEU:HB3	1:A:502:VAL:HG11	1.88	0.55
1:A:568:THR:HG22	1:A:873:VAL:HG21	1.89	0.54
1:A:50:GLU:O	1:A:54:ASN:ND2	2.42	0.52
1:A:410:THR:O	1:A:410:THR:HG23	2.09	0.52
1:A:155:GLU:OE1	1:A:300:HIS:NE2	2.40	0.51
1:A:454:ALA:HA	1:A:509:LEU:HD11	1.91	0.51
1:A:958:SER:OG	2:B:9:ILE:HD11	2.12	0.49
1:A:27:GLY:HA3	4:A:1103:GOL:H12	1.94	0.49
1:A:437:VAL:HG11	1:A:453:TRP:CH2	2.47	0.49
1:A:311:PRO:O	1:A:356:ARG:NH1	2.46	0.49
1:A:1000:THR:HA	1:A:1022:ILE:O	2.14	0.48
2:C:53:GLU:C	2:C:54:LEU:HD12	2.38	0.47
2:B:4:LEU:N	2:B:5:PRO:CD	2.77	0.47
1:A:982:ILE:HG22	1:A:1001:MET:HE1	1.97	0.47
1:A:493:ASN:CB	1:A:517:ILE:HD11	2.40	0.47
2:B:58:LEU:HD11	2:B:101:ILE:HD11	1.97	0.47
1:A:50:GLU:OE2	1:A:451:LYS:NZ	2.36	0.47
1:A:320:ASN:HA	1:A:323:ILE:HD12	1.95	0.46
1:A:590:ARG:CZ	1:A:590:ARG:HB2	2.44	0.46
1:A:634:TYR:OH	1:A:806:PRO:O	2.33	0.46
1:A:650:ASP:O	1:A:654:VAL:HG23	2.16	0.46
1:A:592:PRO:HA	2:B:64:MET:HE3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:544[B]:ASP:O	1:A:545[B]:ASN:HB3	2.16	0.46
1:A:36:THR:O	1:A:36:THR:CG2	2.62	0.46
2:C:121:LEU:HD12	2:C:121:LEU:N	2.30	0.46
1:A:880:GLU:OE2	1:A:895:LYS:N	2.47	0.45
2:B:53:GLU:C	2:B:54:LEU:HD12	2.42	0.45
1:A:588:SER:HA	2:B:1:MET:HG2	1.99	0.45
1:A:50:GLU:HB3	1:A:367:GLY:HA3	1.99	0.45
2:B:1:MET:HE2	2:B:1:MET:HB2	1.91	0.44
1:A:91:ARG:O	1:A:95:THR:OG1	2.34	0.44
2:C:124:ASP:O	2:C:127:GLU:HG2	2.18	0.44
1:A:917:GLY:O	1:A:923:LYS:HG3	2.17	0.44
1:A:1002:ILE:HG23	1:A:1019:PHE:CD2	2.53	0.44
1:A:309:GLU:OE2	1:A:356:ARG:NH2	2.50	0.43
2:B:4:LEU:HD13	2:B:5:PRO:CD	2.48	0.43
2:B:120:PRO:HB3	2:B:126:ALA:CB	2.47	0.43
1:A:410:THR:O	1:A:410:THR:CG2	2.66	0.43
1:A:628:ALA:HA	1:A:816:LEU:HD12	2.00	0.43
1:A:128:ALA:O	1:A:153:SER:HA	2.18	0.43
1:A:381:LYS:O	1:A:382:PHE:HB2	2.19	0.43
1:A:29:GLU:H	4:A:1103:GOL:H31	1.84	0.42
1:A:541:ASN:ND2	1:A:565:GLU:OE2	2.52	0.42
1:A:961:VAL:O	1:A:961:VAL:HG13	2.19	0.42
1:A:435:SER:HB2	1:A:458:LEU:CD1	2.49	0.42
1:A:19:TYR:CG	1:A:31:MET:HE1	2.55	0.41
1:A:22:GLN:OE1	1:A:58:ALA:HA	2.19	0.41
2:C:54:LEU:HD12	2:C:54:LEU:N	2.35	0.41
1:A:641:VAL:HG23	1:A:642:GLU:N	2.35	0.41
1:A:444:ALA:HB2	1:A:481:ARG:HG3	2.01	0.41
1:A:584:GLU:HA	1:A:927:ILE:HD13	2.03	0.41
1:A:160:PHE:CZ	1:A:394:LEU:HD21	2.56	0.41
2:B:120:PRO:HB3	2:B:126:ALA:HB2	2.03	0.41
2:B:41:GLY:HA3	2:B:47:TYR:O	2.21	0.40
2:C:8:ILE:HG21	2:C:32:LEU:HG	2.03	0.40
1:A:313:THR:HG22	1:A:410:THR:HG21	2.04	0.40
2:B:62:TYR:CD1	2:B:63:PRO:HA	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	993/1024 (97%)	942 (95%)	46 (5%)	5 (0%)	24	27
2	B	156/154 (101%)	149 (96%)	6 (4%)	1 (1%)	21	24
2	C	149/154 (97%)	145 (97%)	4 (3%)	0	100	100
All	All	1298/1332 (97%)	1236 (95%)	56 (4%)	6 (0%)	30	27

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	545[A]	ASN
1	A	545[B]	ASN
1	A	746	SER
1	A	703	ASN
2	B	2	ALA
1	A	307	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	879/900 (98%)	831 (94%)	48 (6%)	19	24
2	B	140/136 (103%)	130 (93%)	10 (7%)	13	15
2	C	134/136 (98%)	123 (92%)	11 (8%)	10	11
All	All	1153/1172 (98%)	1084 (94%)	69 (6%)	18	21

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	GLU
1	A	36	THR
1	A	79	GLN
1	A	96	ARG
1	A	120	LEU
1	A	130	ASP
1	A	147	SER
1	A	180	GLU
1	A	196	THR
1	A	248	GLU
1	A	263	LYS
1	A	275	ASN
1	A	281	SER
1	A	294	LEU
1	A	309	GLU
1	A	339	GLU
1	A	349	LYS
1	A	395	GLU
1	A	410	THR
1	A	458	LEU
1	A	517	ILE
1	A	523	GLU
1	A	545[A]	ASN
1	A	545[B]	ASN
1	A	566	SER
1	A	577	VAL
1	A	589	SER
1	A	590	ARG
1	A	591	ASP
1	A	595	LYS
1	A	602	LEU
1	A	618	SER
1	A	637	GLN
1	A	657	SER
1	A	716	THR
1	A	718	LEU
1	A	719	GLU
1	A	745	LYS
1	A	749	SER
1	A	755	VAL
1	A	756	ASP
1	A	815	LYS

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Mol	Chain	Res	Type
1	A	834	ILE
1	A	877	VAL
1	A	880	GLU
1	A	930	ARG
1	A	973	LYS
1	A	1011	GLU
2	B	1	MET
2	B	4	LEU
2	B	20	VAL
2	B	32	LEU
2	B	49	ASP
2	B	55	GLU
2	B	93	THR
2	B	125	VAL
2	B	145	LYS
2	B	151	LYS
2	C	6	LYS
2	C	10	LYS
2	C	18	ASP
2	C	69	VAL
2	C	70	ARG
2	C	82	ARG
2	C	119	ASP
2	C	121	LEU
2	C	125	VAL
2	C	145	LYS
2	C	151	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	89	GLN
1	A	109	ASN
1	A	297	GLN
1	A	301	GLN
1	A	333	GLN
1	A	429	GLN
1	A	493	ASN
1	A	541	ASN
1	A	685	ASN
1	A	686	HIS

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Mol	Chain	Res	Type
1	A	754	ASN
2	C	28	HIS
2	C	118	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	GOL	A	1106	-	5,5,5	0.78	0	5,5,5	1.17	1 (20%)
4	GOL	A	1107	-	5,5,5	0.84	0	5,5,5	1.10	0
3	SO4	A	1102	-	4,4,4	0.23	0	6,6,6	0.15	0
4	GOL	A	1108	-	5,5,5	0.88	0	5,5,5	0.97	0
4	GOL	A	1105	-	5,5,5	0.91	0	5,5,5	1.01	0
3	SO4	A	1101	-	4,4,4	0.24	0	6,6,6	0.11	0
4	GOL	A	1103	-	5,5,5	0.82	0	5,5,5	0.93	0
4	GOL	A	1104	-	5,5,5	0.88	0	5,5,5	1.03	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	1106	-	-	2/4/4/4	-
4	GOL	A	1108	-	-	4/4/4/4	-
4	GOL	A	1105	-	-	3/4/4/4	-
4	GOL	A	1103	-	-	2/4/4/4	-
4	GOL	A	1107	-	-	3/4/4/4	-
4	GOL	A	1104	-	-	2/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1106	GOL	C3-C2-C1	-2.11	104.05	111.80

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1105	GOL	C1-C2-C3-O3
4	A	1107	GOL	C1-C2-C3-O3
4	A	1108	GOL	O1-C1-C2-O2
4	A	1108	GOL	O1-C1-C2-C3
4	A	1103	GOL	O1-C1-C2-O2
4	A	1103	GOL	O1-C1-C2-C3
4	A	1104	GOL	C1-C2-C3-O3
4	A	1106	GOL	O1-C1-C2-C3
4	A	1105	GOL	O2-C2-C3-O3
4	A	1107	GOL	O2-C2-C3-O3
4	A	1104	GOL	O2-C2-C3-O3
4	A	1105	GOL	O1-C1-C2-O2
4	A	1108	GOL	C1-C2-C3-O3
4	A	1106	GOL	O1-C1-C2-O2
4	A	1108	GOL	O2-C2-C3-O3
4	A	1107	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1103	GOL	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	994/1024 (97%)	0.19	19 (1%) 66 71	16, 33, 65, 106	2 (0%)
2	B	152/154 (98%)	0.48	6 (3%) 43 49	19, 43, 65, 93	3 (1%)
2	C	151/154 (98%)	0.86	15 (9%) 13 14	30, 51, 80, 94	0
All	All	1297/1332 (97%)	0.30	40 (3%) 51 58	16, 36, 70, 106	5 (0%)

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	34[A]	TYR	4.0
1	A	544[A]	ASP	3.9
1	A	812	ALA	3.9
1	A	814	PHE	3.8
1	A	747	ASP	3.8
2	C	121	LEU	3.6
2	C	1	MET	3.6
2	C	91	LEU	3.5
2	C	122	ALA	3.5
1	A	749	SER	3.5
2	C	2	ALA	3.1
1	A	339	GLU	3.1
1	A	746	SER	2.7
2	B	43	GLU	2.7
1	A	338	GLY	2.6
1	A	813	GLY	2.6
2	C	18	ASP	2.5
1	A	798	ILE	2.5
1	A	795	SER	2.5
2	C	93	THR	2.5
2	B	57	TYR	2.5
1	A	801	LEU	2.4
2	B	2	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
2	C	134	GLN	2.3
2	C	129	TRP	2.3
2	B	48	GLU	2.3
2	C	65	GLU	2.2
2	C	92	LYS	2.2
2	C	151	LYS	2.2
1	A	797	GLU	2.1
1	A	745	LYS	2.1
1	A	750	ASN	2.1
2	B	30	ASP	2.1
2	C	90	VAL	2.1
1	A	809	SER	2.0
2	C	130	ILE	2.0
1	A	802	VAL	2.0
2	C	64	MET	2.0
1	A	116	ASP	2.0
1	A	748	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	A	1103	6/6	0.78	0.15	34,42,51,53	0
4	GOL	A	1105	6/6	0.87	0.10	27,33,37,38	0
4	GOL	A	1108	6/6	0.88	0.21	36,44,49,49	0
3	SO4	A	1102	5/5	0.91	0.10	31,31,35,39	0
4	GOL	A	1104	6/6	0.92	0.10	35,42,48,49	0
4	GOL	A	1107	6/6	0.94	0.11	27,34,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	A	1106	6/6	0.94	0.10	18,25,32,33	0
3	SO4	A	1101	5/5	0.98	0.05	29,31,33,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.